STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

**The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:**

Application Serial Number: _/o/5 S0, 498A_____

Source: _____/FWO_____

Date Processed by STIC: _____3/2 4/06_____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY** or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY**
**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER
VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
   User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/550, 498A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length — The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3____Misaligned Amino
Numbering — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
(OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences
(NEW RULES) — Sequence(s) _____ missing. **If intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>
Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11____Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12____PatentIn 2.0
"bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa — "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06
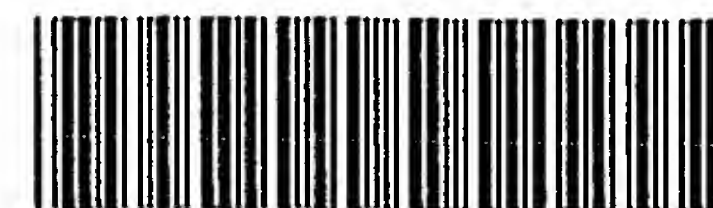
IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/550,498A

DATE: 03/24/2006
TIME: 17:41:40

Input Set : **A:\persico corrected feb06.ST25.txt**
Output Set: **N:\CRF4\03242006\J550498A.raw**

```
 3 <110> APPLICANT: Minchiotti, Gabriella
 4        Persico, Maria
 5        Parisi, Silvia
 7 <120> TITLE OF INVENTION: METHOD FOR PROMOTING DIFFERENTIATION OF STAMINAL CELL
 9 <130> FILE REFERENCE: AE 89363
11 <140> CURRENT APPLICATION NUMBER: US 10/550,498A
12 <141> CURRENT FILING DATE: 2005-09-20
14 <160> NUMBER OF SEQ ID NOS: 42
16 <170> SOFTWARE: PatentIn version 3.3
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 22
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial
23 <220> FEATURE:
24 <223> OTHER INFORMATION: primer nodal F
27 <220> FEATURE:
28 <221> NAME/KEY: primer_bind
29 <222> LOCATION: (1)..(22)
31 <400> SEQUENCE: 1
32 ttccttctca ggtcacgttt gc                                        22
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 21
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial
40 <220> FEATURE:
41 <223> OTHER INFORMATION: Primer nodal R
44 <220> FEATURE:
45 <221> NAME/KEY: primer_bind
46 <222> LOCATION: (1)..(21)
48 <400> SEQUENCE: 2
49 ggtggggttg gtatcgtttc a                                         21
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 25
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial
57 <220> FEATURE:
58 <223> OTHER INFORMATION: primer alk-4 F
61 <220> FEATURE:
62 <221> NAME/KEY: primer_bind
63 <222> LOCATION: (1)..(25)
65 <400> SEQUENCE: 3
66 aaggatccag gctctgctgt gtgcc                                     25
69 <210> SEQ ID NO: 4
```

RAW SEQUENCE LISTING   DATE: 03/24/2006
PATENT APPLICATION: **US/10/550,498A**   TIME: 17:41:40

Input Set : **A:\persico corrected feb06.ST25.txt**
Output Set: **N:\CRF4\03242006\J550498A.raw**

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 70 <211> LENGTH: 26
 71 <212> TYPE: DNA
 72 <213> ORGANISM: Artificial
 74 <220> FEATURE:
 75 <223> OTHER INFORMATION: primer alk-4 R
 78 <220> FEATURE:
 79 <221> NAME/KEY: primer_bind
 80 <222> LOCATION: (1)..(26)
 82 <400> SEQUENCE: 4
 83 acggatccat gtccaacctc tggcgg                              26
 86 <210> SEQ ID NO: 5
 87 <211> LENGTH: 20
 88 <212> TYPE: DNA
 89 <213> ORGANISM: Artificial
 91 <220> FEATURE:
 92 <223> OTHER INFORMATION: primer ActRIIB F
 95 <220> FEATURE:
 96 <221> NAME/KEY: primer_bind
 97 <222> LOCATION: (1)..(20)
 99 <400> SEQUENCE: 5
100 atgtgccgtg gtgtcgtggt                                    20
103 <210> SEQ ID NO: 6
104 <211> LENGTH: 20
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial
108 <220> FEATURE:
109 <223> OTHER INFORMATION: primer ActRIIB R
112 <220> FEATURE:
113 <221> NAME/KEY: primer_bind
114 <222> LOCATION: (1)..(20)
116 <400> SEQUENCE: 6
117 gacctcctga tcagggatac                                    20
120 <210> SEQ ID NO: 7
121 <211> LENGTH: 24
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial
125 <220> FEATURE:
126 <223> OTHER INFORMATION: primer MLC2v F
129 <220> FEATURE:
130 <221> NAME/KEY: primer_bind
131 <222> LOCATION: (1)..(24)
133 <400> SEQUENCE: 7
134 gccaagaagc ggatagaagg cggg                               24
137 <210> SEQ ID NO: 8
138 <211> LENGTH: 24
139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial
142 <220> FEATURE:
143 <223> OTHER INFORMATION: primer MLC2v R
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RAW SEQUENCE LISTING   DATE: 03/24/2006
PATENT APPLICATION: US/10/550,498A   TIME: 17:41:40

Input Set : **A:\persico corrected feb06.ST25.txt**
Output Set: **N:\CRF4\03242006\J550498A.raw**

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146 <220> FEATURE:
147 <221> NAME/KEY: primer_bind
148 <222> LOCATION: (1)..(24)
150 <400> SEQUENCE: 8
151 ctgtggttca gggctcagtc cttc                                24
154 <210> SEQ ID NO: 9
155 <211> LENGTH: 24
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial
159 <220> FEATURE:
160 <223> OTHER INFORMATION: primer cardiac alphaMHC F
163 <220> FEATURE:
164 <221> NAME/KEY: primer_bind
165 <222> LOCATION: (1)..(24)
167 <400> SEQUENCE: 9
168 ggaagagtga gcggcgcatc aagg                                24
171 <210> SEQ ID NO: 10
172 <211> LENGTH: 22
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial
176 <220> FEATURE:
177 <223> OTHER INFORMATION: primer cardiac alphaMHC R
180 <220> FEATURE:
181 <221> NAME/KEY: primer_bind
182 <222> LOCATION: (1)..(22)
184 <400> SEQUENCE: 10
185 ctgctggaga ggttattcct cg                                  22
188 <210> SEQ ID NO: 11
189 <211> LENGTH: 25
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial
193 <220> FEATURE:
194 <223> OTHER INFORMATION: primer HPRT F
197 <220> FEATURE:
198 <221> NAME/KEY: primer_bind
199 <222> LOCATION: (1)..(25)
201 <400> SEQUENCE: 11
202 cctgctggat tacattaaag cactg                               25
205 <210> SEQ ID NO: 12
206 <211> LENGTH: 25
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial
210 <220> FEATURE:
211 <223> OTHER INFORMATION: primer HPRT R
214 <220> FEATURE:
215 <221> NAME/KEY: primer_bind
216 <222> LOCATION: (1)..(25)
218 <400> SEQUENCE: 12
219 cctgaagtac tcattatagt caagg                               25
```

RAW SEQUENCE LISTING   DATE: 03/24/2006
PATENT APPLICATION: US/10/550,498A   TIME: 17:41:40

Input Set : A:\persico corrected feb06.ST25.txt
Output Set: N:\CRF4\03242006\J550498A.raw

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222 <210> SEQ ID NO: 13
223 <211> LENGTH: 27
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial
227 <220> FEATURE:
228 <223> OTHER INFORMATION: mut Asn63-Ile
231 <220> FEATURE:
232 <221> NAME/KEY: primer_bind
233 <222> LOCATION: (1)..(27)
235 <400> SEQUENCE: 13
236 gtaagtcgct tattaaaact tgctgtc                               27
239 <210> SEQ ID NO: 14
240 <211> LENGTH: 27
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial
244 <220> FEATURE:
245 <223> OTHER INFORMATION: mut Asn63-Ile
248 <220> FEATURE:
249 <221> NAME/KEY: primer_bind
250 <222> LOCATION: (1)..(27)
252 <400> SEQUENCE: 14
253 gacagcaagt tttaataagc gacttac                               27
256 <210> SEQ ID NO: 15
257 <211> LENGTH: 38
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial
261 <220> FEATURE:
262 <223> OTHER INFORMATION: mut Gly71-Asn
265 <220> FEATURE:
266 <221> NAME/KEY: primer_bind
267 <222> LOCATION: (1)..(38)
269 <400> SEQUENCE: 15
270 cttgctgtct gaatggaaac acttgcatcc tggggtcc                   38
273 <210> SEQ ID NO: 16
274 <211> LENGTH: 38
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial
278 <220> FEATURE:
279 <223> OTHER INFORMATION: mut Gly71-Asn
282 <220> FEATURE:
283 <221> NAME/KEY: primer_bind
284 <222> LOCATION: (1)..(38)
286 <400> SEQUENCE: 16
287 ggaccccagg atgcaagtgt ttccattcag acagcaag                   38
290 <210> SEQ ID NO: 17
291 <211> LENGTH: 23
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial
295 <220> FEATURE:
```

This does not explain the source of genetic material in the sequence. See item 11 on Error summary sheet.

same error

RAW SEQUENCE LISTING   DATE: 03/24/2006
PATENT APPLICATION: US/10/550,498A   TIME: 17:41:40

Input Set : A:\persico corrected feb06.ST25.txt
Output Set: N:\CRF4\03242006\J550498A.raw

```
296 <223> OTHER INFORMATION: mut Thr72-Ala
299 <220> FEATURE:
300 <221> NAME/KEY: primer_bind
301 <222> LOCATION: (1)..(23)
303 <400> SEQUENCE: 17
304 gaatggaggg gcttgcatcc tgg                                    23
307 <210> SEQ ID NO: 18
308 <211> LENGTH: 23
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial
312 <220> FEATURE:
313 <223> OTHER INFORMATION: mut Thr72-Ala
316 <220> FEATURE:
317 <221> NAME/KEY: primer_bind
318 <222> LOCATION: (1)..(23)
320 <400> SEQUENCE: 18
321 ccaggatgca agcccctcca ttc                                    23
324 <210> SEQ ID NO: 19
325 <211> LENGTH: 29
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial
329 <220> FEATURE:
330 <223> OTHER INFORMATION: mut Ser77-Ala
333 <220> FEATURE:
334 <221> NAME/KEY: primer_bind
335 <222> LOCATION: (1)..(29)
337 <400> SEQUENCE: 19
338 cttgcatcct gggggccttc tgtgcctgc                              29
341 <210> SEQ ID NO: 20
342 <211> LENGTH: 29
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial
346 <220> FEATURE:
347 <223> OTHER INFORMATION: mut Ser77-Ala
350 <220> FEATURE:
351 <221> NAME/KEY: primer_bind
352 <222> LOCATION: (1)..(29)
354 <400> SEQUENCE: 20
355 gcaggcacag aaggccccca ggatgcaag                              29
358 <210> SEQ ID NO: 21
359 <211> LENGTH: 31
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial
363 <220> FEATURE:
364 <223> OTHER INFORMATION: mut Phe78-Ala
367 <220> FEATURE:
368 <221> NAME/KEY: primer_bind
369 <222> LOCATION: (1)..(31)
371 <400> SEQUENCE: 21
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Please correct these types of errors in subsequent sequences

6

VERIFICATION SUMMARY   DATE: 03/24/2006
PATENT APPLICATION: US/10/550,498A   TIME: 17:41:41

Input Set : **A:\persico corrected feb06.ST25.txt**
Output Set: **N:\CRF4\03242006\J550498A.raw**